SEQUENCE LISTING

<110> Kloek, Andrew
       Williams, Deryck Jeremy
       Salmon, Brandy

<120> NEMATODE GS-LIKE SEQUENCES

<130> 12557-004001

<150> US 60/276,621
<151> 2001-03-16

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1471
<212> DNA
<213> Meloidogyne incognita

<220>
<221> CDS
<222> (34)...(1395)

<400> 1

```
tgtataataa agcttcataa tataaaattt taa atg acc atc act tat gat gaa        54
                                     Met Thr Ile Thr Tyr Asp Glu
                                      1                   5

cta aat aat ttg att aga aat gga aaa att gac acg gta gtt ttg gca       102
Leu Asn Asn Leu Ile Arg Asn Gly Lys Ile Asp Thr Val Val Leu Ala
         10                  15                  20

tgc gtc gac atg caa ggc cgg ctg atg ggc aag aga tta act ggg cgt      150
Cys Val Asp Met Gln Gly Arg Leu Met Gly Lys Arg Leu Thr Gly Arg
     25                  30                  35

cat ttt tta gga ttg gat caa aag aag att agc att agc acg ttt gta      198
His Phe Leu Gly Leu Asp Gln Lys Lys Ile Ser Ile Ser Thr Phe Val
 40                  45                  50                  55

tat gcg gta act ata gaa ggc atc gct ggc gga ggt tat gag atc tca      246
Tyr Ala Val Thr Ile Glu Gly Ile Ala Gly Gly Gly Tyr Glu Ile Ser
                 60                  65                  70

agt gta gac aca ggt tat agt gat tgt cat ctc tgt gca gat ttg aat      294
Ser Val Asp Thr Gly Tyr Ser Asp Cys His Leu Cys Ala Asp Leu Asn
                 75                  80                  85

tcc ctt cat tta ctc ccg tgg tca gaa ggc gct gta ttg gca att tcc      342
Ser Leu His Leu Leu Pro Trp Ser Glu Gly Ala Val Leu Ala Ile Ser
             90                  95                 100
```

```
aat cct cat aat ttc gtt act tct gag cca ttg ttc tgt tct cct cga        390
Asn Pro His Asn Phe Val Thr Ser Glu Pro Leu Phe Cys Ser Pro Arg
    105                 110                 115

gta ata ctc atg cag caa att gag cgc ctg gct aat cta aag ctt aaa        438
Val Ile Leu Met Gln Gln Ile Glu Arg Leu Ala Asn Leu Lys Leu Lys
120                 125                 130                 135

ggc ctt ttt gct tct gaa cta gaa ttt aat ctt ttc aac gaa act tat        486
Gly Leu Phe Ala Ser Glu Leu Glu Phe Asn Leu Phe Asn Glu Thr Tyr
                140                 145                 150

aag agt gcc agc caa aag cat tgg aaa aat tta aaa acc gcg cag cct        534
Lys Ser Ala Ser Gln Lys His Trp Lys Asn Leu Lys Thr Ala Gln Pro
                155                 160                 165

cat cat caa tgg atg aat att agt gca agt agt ggg att gaa act ttt        582
His His Gln Trp Met Asn Ile Ser Ala Ser Ser Gly Ile Glu Thr Phe
            170                 175                 180

atg cgt tct gtg cgt aat aaa tta gaa gaa gcc ggt att ttg atg gag        630
Met Arg Ser Val Arg Asn Lys Leu Glu Glu Ala Gly Ile Leu Met Glu
    185                 190                 195

gcg aca cat ccc gaa ttt tta cct agt cag cat gaa ctt aat ttt gta        678
Ala Thr His Pro Glu Phe Leu Pro Ser Gln His Glu Leu Asn Phe Val
200                 205                 210                 215

cca gcc gat cct cta aca atg gca gat cgt cat att att gca aaa cat        726
Pro Ala Asp Pro Leu Thr Met Ala Asp Arg His Ile Ile Ala Lys His
                220                 225                 230

gga gtt cgc gaa atg gca gaa cag tct gga atg gtt gca act ttt atg        774
Gly Val Arg Glu Met Ala Glu Gln Ser Gly Met Val Ala Thr Phe Met
            235                 240                 245

gct aaa ttg agt tca act gcg ctt ggt aat gcc tgc cat att cat atg        822
Ala Lys Leu Ser Ser Thr Ala Leu Gly Asn Ala Cys His Ile His Met
            250                 255                 260

tca ctt caa gat gca gaa aca gaa aaa aat gca ttt tat gat caa aac        870
Ser Leu Gln Asp Ala Glu Thr Glu Lys Asn Ala Phe Tyr Asp Gln Asn
    265                 270                 275

gat gaa tat gga atg tca acc tta gct cgt aat tgg att gct gga tta        918
Asp Glu Tyr Gly Met Ser Thr Leu Ala Arg Asn Trp Ile Ala Gly Leu
280                 285                 290                 295

ttg aaa tac gta cct gaa gcg act tat ttc ttt gca tct tac atc aac        966
Leu Lys Tyr Val Pro Glu Ala Thr Tyr Phe Phe Ala Ser Tyr Ile Asn
                300                 305                 310

tcg tac aaa aga ctt caa ccg ctt act ttt gcg cca aca aaa tgt tgt       1014
Ser Tyr Lys Arg Leu Gln Pro Leu Thr Phe Ala Pro Thr Lys Cys Cys
            315                 320                 325
```

```
tgg gca att gac aac cga aca agc gcc ttt cga ctt tgt aat tca aaa      1062
Trp Ala Ile Asp Asn Arg Thr Ser Ala Phe Arg Leu Cys Asn Ser Lys
        330             335             340

tcc gag gga att aat gtt gag ctg cgt att ggt ggc gct gat ttg aac      1110
Ser Glu Gly Ile Asn Val Glu Leu Arg Ile Gly Gly Ala Asp Leu Asn
        345             350             355

cct tat tta gct ttt tcc gca atc ata gct gca gga att agc ggt ata      1158
Pro Tyr Leu Ala Phe Ser Ala Ile Ile Ala Ala Gly Ile Ser Gly Ile
360             365             370             375

gaa gaa aag ctt gaa ctt ccc cct cct gca tct ggc aat gtt tac aat      1206
Glu Glu Lys Leu Glu Leu Pro Pro Pro Ala Ser Gly Asn Val Tyr Asn
            380             385             390

gat aag gaa tta cct gaa ttt cct aat tcc tta caa aat gct aca cat      1254
Asp Lys Glu Leu Pro Glu Phe Pro Asn Ser Leu Gln Asn Ala Thr His
            395             400             405

ctt cta aaa gaa tcg aaa atg ctg aat aaa aca ttc ggg gag aag ttg      1302
Leu Leu Lys Glu Ser Lys Met Leu Asn Lys Thr Phe Gly Glu Lys Leu
            410             415             420

att cta cat tat gta aac gct gct aat gtt gag att aat gaa ttt tca      1350
Ile Leu His Tyr Val Asn Ala Ala Asn Val Glu Ile Asn Glu Phe Ser
            425             430             435

aaa caa gtt act gac tgg gag ctt aat caa gga ttt aat aga tat          1395
Lys Gln Val Thr Asp Trp Glu Leu Asn Gln Gly Phe Asn Arg Tyr
440             445             450

taatatttta atgcttatgt agataacaat caaaatata atctttaaat acataattaa     1455
aaaaaaaaaa aaaaaa                                                     1471
```

<210> 2
<211> 454
<212> PRT
<213> Meloidogyne incognita

<400> 2
```
Met Thr Ile Thr Tyr Asp Glu Leu Asn Asn Leu Ile Arg Asn Gly Lys
 1               5              10                  15
Ile Asp Thr Val Val Leu Ala Cys Val Asp Met Gln Gly Arg Leu Met
            20              25              30
Gly Lys Arg Leu Thr Gly Arg His Phe Leu Gly Leu Asp Gln Lys Lys
        35              40              45
Ile Ser Ile Ser Thr Phe Val Tyr Ala Val Thr Ile Glu Gly Ile Ala
    50              55              60
Gly Gly Gly Tyr Glu Ile Ser Ser Val Asp Thr Gly Tyr Ser Asp Cys
65              70              75              80
His Leu Cys Ala Asp Leu Asn Ser Leu His Leu Leu Pro Trp Ser Glu
            85              90              95
Gly Ala Val Leu Ala Ile Ser Asn Pro His Asn Phe Val Thr Ser Glu
            100             105             110
Pro Leu Phe Cys Ser Pro Arg Val Ile Leu Met Gln Gln Ile Glu Arg
    115             120             125
```

```
Leu Ala Asn Leu Lys Leu Lys Gly Leu Phe Ala Ser Glu Leu Glu Phe
    130             135             140
Asn Leu Phe Asn Glu Thr Tyr Lys Ser Ala Ser Gln Lys His Trp Lys
145                 150             155                 160
Asn Leu Lys Thr Ala Gln Pro His His Gln Trp Met Asn Ile Ser Ala
            165             170                 175
Ser Ser Gly Ile Glu Thr Phe Met Arg Ser Val Arg Asn Lys Leu Glu
        180             185                 190
Glu Ala Gly Ile Leu Met Glu Ala Thr His Pro Glu Phe Leu Pro Ser
        195             200             205
Gln His Glu Leu Asn Phe Val Pro Ala Asp Pro Leu Thr Met Ala Asp
    210             215             220
Arg His Ile Ile Ala Lys His Gly Val Arg Glu Met Ala Glu Gln Ser
225             230             235             240
Gly Met Val Ala Thr Phe Met Ala Lys Leu Ser Ser Thr Ala Leu Gly
            245             250             255
Asn Ala Cys His Ile His Met Ser Leu Gln Asp Ala Glu Thr Glu Lys
            260             265             270
Asn Ala Phe Tyr Asp Gln Asn Asp Glu Tyr Gly Met Ser Thr Leu Ala
            275             280             285
Arg Asn Trp Ile Ala Gly Leu Leu Lys Tyr Val Pro Glu Ala Thr Tyr
    290             295             300
Phe Phe Ala Ser Tyr Ile Asn Ser Tyr Lys Arg Leu Gln Pro Leu Thr
305             310             315             320
Phe Ala Pro Thr Lys Cys Cys Trp Ala Ile Asp Asn Arg Thr Ser Ala
            325             330             335
Phe Arg Leu Cys Asn Ser Lys Ser Glu Gly Ile Asn Val Glu Leu Arg
            340             345             350
Ile Gly Gly Ala Asp Leu Asn Pro Tyr Leu Ala Phe Ser Ala Ile Ile
            355             360             365
Ala Ala Gly Ile Ser Gly Ile Glu Glu Lys Leu Glu Leu Pro Pro Pro
    370             375             380
Ala Ser Gly Asn Val Tyr Asn Asp Lys Glu Leu Pro Glu Phe Pro Asn
385             390             395             400
Ser Leu Gln Asn Ala Thr His Leu Leu Lys Glu Ser Lys Met Leu Asn
            405             410             415
Lys Thr Phe Gly Glu Lys Leu Ile Leu His Tyr Val Asn Ala Ala Asn
            420             425             430
Val Glu Ile Asn Glu Phe Ser Lys Gln Val Thr Asp Trp Glu Leu Asn
    435             440             445
Gln Gly Phe Asn Arg Tyr
    450
```

```
<210> 3
<211> 1362
<212> DNA
<213> Meloidogyne incognita

<400> 3
atgaccatca cttatgatga actaaataat ttgattagaa atggaaaaat tgacacggta    60
gttttggcat gcgtcgacat gcaaggccgg ctgatgggca agagattaac tggcgtcat   120
tttttaggat tggatcaaaa gaagattagc attagcacgt ttgtatatgc ggtaactata   180
gaaggcatcg ctggcggagg ttatgagatc tcaagtgtag acacaggtta tagtgattgt   240
catctctgtg cagatttgaa ttcccttcat ttactcccgt ggtcagaagg cgctgtattg   300
gcaatttcca atcctcataa tttcgttact tctgagccat tgttctgttc tcctcgagta   360
atactcatgc agcaaattga gcgcctggct aatctaaagc ttaaaggcct ttttgcttct   420
gaactagaat ttaatctttt caacgaaact tataagagtg ccagccaaaa gcattggaaa   480
```

```
aatttaaaaa ccgcgcagcc tcatcatcaa tggatgaata ttagtgcaag tagtgggatt    540
gaaactttta tgcgttctgt gcgtaataaa ttagaagaag ccggtatttt gatggaggcg    600
acacatcccg aattttacc  tagtcagcat gaacttaatt ttgtaccagc cgatcctcta    660
acaatggcag atcgtcatat tattgcaaaa catggagttc gcgaaatggc agaacagtct    720
ggaatggttg caacttttat ggctaaattg agttcaactg cgcttggtaa tgcctgccat    780
attcatatgt cacttcaaga tgcagaaaca gaaaaaaatg cattttatga tcaaaacgat    840
gaatatggaa tgtcaacctt agctcgtaat tggattgctg gattattgaa atacgtacct    900
gaagcgactt atttctttgc atcttacatc aactcgtaca aaagacttca accgcttact    960
tttgcgccaa caaaatgttg ttgggcaatt gacaaccgaa caagcgcctt tcgactttgt   1020
aattcaaaat ccgagggaat taatgttgag ctgcgtattg gtggcgctga tttgaaccct   1080
tatttagctt tttccgcaat catagctgca ggaattagcg gtatagaaga aaagcttgaa   1140
cttcccccctc ctgcatctgg caatgtttac aatgataagg aattacctga atttcctaat   1200
tccttacaaa atgctacaca tcttctaaaa gaatcgaaaa tgctgaataa aacattcggg   1260
gagaagttga ttctacatta tgtaaacgct gctaatgttg agattaatga attttcaaaa   1320
caagttactg actgggagct taatcaagga tttaatagat at                      1362
```

<210> 4
<211> 457
<212> PRT
<213> Mycobacterium tuberculosis

<400> 4

```
Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg
 1               5                  10                  15
Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp
            20                  25                  30
Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
        35                  40                  45
Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
    50                  55                  60
Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
65                  70                  75                  80
Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
                85                  90                  95
Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
            100                 105                 110
Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
        115                 120                 125
Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
    130                 135                 140
Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
145                 150                 155                 160
Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
                165                 170                 175
Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
            180                 185                 190
Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
        195                 200                 205
Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu
    210                 215                 220
Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
225                 230                 235                 240
Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
                245                 250                 255
Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
            260                 265                 270
```

```
Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
        275                 280                 285
Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg
        290                 295                 300
Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe
305                 310                 315                 320
Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
                325                 330                 335
Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
            340                 345                 350
Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
            355                 360                 365
Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
        370                 375                 380
Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
385                 390                 395                 400
Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
                405                 410                 415
Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
            420                 425                 430
Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
            435                 440                 445
Glu Arg Ile Arg Gly Phe Glu Arg Leu
450                 455
```

```
<210> 5
<211> 22
<212> DNA
<213> vector polylinker primer

<400> 5
gtaatacgac tcactatagg gc                                              22

<210> 6
<211> 20
<212> DNA
<213> vector polylinker primer

<400> 6
aattaaccct cactaaaggg                                                 20

<210> 7
<211> 49
<212> DNA
<213> universal primer to poly A tail

<400> 7
gagagagaga gagagagaga actagtctcg agtttttttt tttttttttt               49

<210> 8
<211> 22
<212> DNA
<213> Nematode transpliced leader

<400> 8
gggtttaatt acccaagttt ga                                             22
```

<210> 9
<211> 21
<212> DNA
<213> Meloidogyne incognita GS

<400> 9
aagtcgaaag gcgcttgttc g   21